Two Generalizations of the Design of Experiments Methodology for Enhanced Process Understanding

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Machine Learning Algorithms for Chemical Reaction Systems

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Types of Models

Knowledge-Driven Models Instead of "Fundamental" or "First Principles" Data-Driven Models No knowledge of Inner Workings of Process Hybrid Models Partial Knowledge + Data Models Should Have a Purpose Models for Kinetics, Process Design, Optimization, Control Conceptual, Physical (Pilot Plant), Mathematical, ...



Plethora of Robotic Devices





If You have One ... Million \$

The Age of Big Data





Design Experiments - Analyze Data

Design of Experiments (DoE)

- Very Powerful Methodology 50 Years Young!
- Never Change One Condition at a time
- Full Factorial Designs,
- Fractional Factorial Designs,
- 1/2 fraction: 2ⁿ⁻¹
- 1/4 fraction: 2ⁿ⁻²
- 1/8 fraction: 2ⁿ⁻³
- Center Composite Design



Is DoE Sufficient?

My Answer is: **NO**



1st Generalization: DoE → DoDE

Time-Varying Inputs (Factors)
 Design of Dynamic Experiments (DoDE)
 Batch Reactor Temperate vs. Time, T(t)=?
 Feeding of Bioreactor with Sugar Source, u(t)=?
 Bioreactor pH vs. Time, pH(t)=?
 How Many Dynamic Experiments?
 How we Design them?

Georgakis, C., (2013) "Design of Dynamic Experiments: A Data-Driven Methodology for the Optimization of Time-Varying Processes" Ind. Eng. Chem. Res. **52** (35):12369-12382

2nd Generalization: RSM -> DRSM

Tufts

RSM: Response Surface Methodology Interpolative Polynomial Model of Output Composition Measurements every Hour ► For/12 hrs → 12 RSMs ?? **DRSM:** Dynamic Response Surface Method $y(t) = \beta_0(t) + \sum_{i=1}^n \beta_i(t) X_i +$ $\sum_{i=1}^{n} \sum_{j=i+1}^{n} \beta_{ij}(t) X_i X_j + \sum_{i=1}^{n} \beta_{ii}(t) X_i^2$ $\beta_{q}(t) = \gamma_{q,1}P_{0}(t) + \gamma_{q,2}P_{1}(t) + \cdots + \gamma_{q,R}P_{R-1}(t)$ $P_i(t)$ the ith Shifted Legendre Polynomial $P_0 = 1$, $P_1(t) = -1 + 2t$, $P_2(t) = 1 - 6t + 6t^2$



DoDE: Time-Varying Inputs

Define Time-Varying Input Domain
 Define Time-Varying Coded Variable, z(τ)

$$u_{0}(\tau) = \frac{u_{\max}(\tau) + u_{\min}(\tau)}{2}$$
$$\Delta u(\tau) = \frac{u_{\max}(\tau) - u_{\min}(\tau)}{2}$$
$$z(\tau) = \frac{u(\tau) - u_{0}(\tau)}{\Delta u(\tau)}$$
$$-1 \le z(\tau) \le +1, \quad \tau = t / t_{b}$$
$$u(\tau) \triangleq u_{0}(\tau) + \Delta u(\tau)z(\tau)$$



Main Idea: $z(\tau) = a_1 P_0(\tau) + a_2 P_1(\tau) + a_3 P_2(\tau) + \cdots$





DODE Example: Batch Reactor **Reversible Reaction in Batch** $A_1 \rightleftharpoons A_2 (15 < T < 50 \circ C)$ $r = k_1 A_1 - k_2 A_2$ $k_i = k_{i0} \exp\left(-\frac{E_i}{RT}\right)$ with $E_2 > E_1$

Model-based Optimum Conversion: Decreasing Temperature Profile

74.6%







DoDE Semi-Batch Reactor

Reaction Example:

 $\begin{array}{ll} Rxn1: \ A+B \longrightarrow C & r_1 = k_1 C_A C_B, k_1 = 2 \ l \ mol^{-1} h^{-1} \\ Rxn2: \ 2B \longrightarrow D, & r_2 = k_2 C_B^2, \ k_2 = 1 \ l \ mol^{-1} h^{-1} \\ Rxn3: & C \longrightarrow E, & r_1 = k_3 C_C, \ k_3 = 1 \ h^{-1} \end{array}$





DoDE: The Dow Project



Polymerization → Increase Productivity
 NO Detailed Knowledge-Driven Process Model
 Inputs (factors) Can Vary with Time



15 DoDE experiments → Batch Time Reduced by 20% **Productivity Increase by 20%**



The DRSM Idea

From RSM:

• $y = \beta_0 + \sum_{i=1}^n \beta_i X_i + \sum_{i=1}^n \sum_{j=i+1}^n \beta_{ij} X_i X_j + \sum_{i=1}^n \beta_{ii} X_i^2$

To DRSM:

• $y(t) = \beta_0(t) + \sum_{i=1}^n \beta_i(t) X_i + \sum_{i=1}^n \sum_{j=i+1}^n \beta_{ij}(t) X_i X_j + \sum_{i=1}^n \beta_{ii}(t) X_i^2$

Parameterization:

$$\beta_{q}(t) = \gamma_{q,1}P_{0}(t) + \gamma_{q,2}P_{1}(t) + \cdots \gamma_{q,R}P_{R-1}(t)$$

• $q = i, ij, or ii \text{ with } i, j = 1, 2, ..., n; j < i$

R(parameters) < K(Data per Experiment)</p> **DRSM-1: Parametrization with t** Has Oscillations **DRSM-2: Parametrization with** $\theta = \left\{1 - \exp\left(-\frac{t}{t_0}\right)\right\}$

 $\bullet \ 0 \le t < \infty \iff 0 \le \theta < 1$

NO Oscillations - Excellent Model



DRSM-2c for **ALL** Pfizer Data: $C_1(t)$

Time-Resolved Species 1 Measurements with
 y(t) = β₀(t) + Σⁿ_{i=1} β_i(t)X_i + Σⁿ_{i=1} Σⁿ_{j=i+1} β_{ij}(t)X_iX_j + Σⁿ_{i=1} β_{ii}(t)X²_i
 R = 3, t_c = 3.3 All 17 experiments





DRSM-2c for **ALL** Pfizer Data: $C_5(t)$

Species 5: $R = 5, t_c = 5.4$





DRSM-2c for **ALL** Pfizer Data: $C_7(t)$

Species 7: $R = 3, t_c = 5.4$





DRSM-2c: Missing Pfizer Data: C1()







DRSM-2c: Missing Pfizer Data: $C_5(\dagger)$

Species 5: R=3 Tc=3.3





DRSM-2c: Missing Pfizer Data: C7()

Species 7: R=3 Tc=3.3



DRSM-2 vs DRSM-1 - Non-equidistant Data





Species E with Prediction Interval





Fractional Factorial Design (Merck)

3 Species and 5 Factors: A, B, C, D, and E
2 Blocks: Robotic & Manual
6 Data/Batch at *Unequal* Intervals
0, 20, 40, 60, 120, 240 mins
LC area converted to concentration

The 5 FACTORS

A: Methanol ratio, (% wt/wt solvent)
B: Starting material, wt%
D: Water wt%
C: Base, wt%
E: Temperature

¹/₄ Fractional factorial design: 2⁵⁻² design

- 8 experiments
- Aliasing Structure: D = AB, and E = AC



2FI Model: Species B

LoF p-value = 0.99 → Perfect model



 $\tilde{y}(t) = \beta_0(t) + \beta_A(t)A + \beta_B(t)B + \beta_C(t)C + \beta_D(t)D + \beta_E(t)E + \beta_{BC}(t)BC + \beta_{CD}(t)CD$



2FI Model: Species A

LoF p-value = 0.99 → Perfect model





2FI Model: Species C

LoF p-value = 0.06 → Good Model



Block Effect Insignificant: Robotic vs. Manual Operation



Rate Data \Rightarrow Stoichiometry

 $Rxn1: A + B \rightarrow C$ $Rxn2: 2B \rightarrow D$ Rates of appearance for Each Species $Rxn3: C \rightarrow E$ For $n_{K} = 100$ matrix D_{k} is a 100×5 Data Matrix for Rates of ALL Species and ALL Experiments: R_c $\mathbf{R}_{c} = \begin{pmatrix} \mathbf{D}_{1} \\ \mathbf{D}_{2} \\ \vdots \\ \mathbf{D}_{k} \end{pmatrix} D_{k} = \text{Data from } k\text{-th experiment} \\ k = 1, 2, \dots, n_{e}$ For $n_e = 9$ experiments R_c is a 900×5 matrix Number of SVD=Singular Value Decomposition of R_c Significant SVs = ? $\mathbf{P} \mathbf{R}_{c} = \mathbf{U} \boldsymbol{\Sigma} \mathbf{V}^{\mathrm{T}}, \ \boldsymbol{\Sigma} = \begin{pmatrix} \sigma_{1} & 0 & 0 \\ 0 & \ddots & 0 \\ 0 & 0 & \sigma_{\mathrm{T}} \end{pmatrix}, \ \mathbf{U} \boldsymbol{\Sigma} \mathbf{V}^{\mathrm{T}} \ sizes: 900X5, 5X5 \& 5X5 \end{pmatrix}$



SVD: $R_c = U\Sigma V^{T}$ & Projections

• # of Reactions \Leftrightarrow Significant σ_i Values= 3

•
$$R_c = U_3 \Sigma_3 V_3^T$$
 $V_3^T = \begin{pmatrix} v_1^T \\ v_2^T \\ v_3^T \end{pmatrix} = \begin{pmatrix} 0.41 & 0.84 & -0.26 & -0.21 & -0.15 \\ -0.26 & 0.21 & 0.79 & -0.23 & 0.50 \\ 0.60 & -0.28 & 0.01 & 0.44 & -0.61 \end{pmatrix}$
• **IS (-1,-1,1,0,0) a Linear Combination of the V_3^T rows ?**
• Projection Matrix: $P = V_3^T V_3$
• Projection of Candidate Stoichiometry: $n_{ir} = n_i V_3^T V_3$
• It TRUE that: $n_{ir} \cong n_i$?

Projection Score: $PS = 100\{1 - ||n_{ir} - n_i|| / ||n_i||\}$ ■ PS ≥ 90 is GOOD



Initial & Sequential Projections

PREPARATION of Data - Rate Data Matrix \mathbf{R}_c of size $n_d \times n_s$ $n_d = \#$ of Data, $n_s = \#$ of species Number of Significant Singular Values (sSVs) Statistical Determination via an *F*-test = n_{ssvs} Malinowski, J. of Chemometrics. 1989; 3(1):49-60 Define Candidate Stoichiometries **INITIAL** Projection Step Calculate Projection Scores (PC) - Accept n_i Reactions with PC \geq 90 Subtract from Rate Data Contribution of Identified Rxns **SEQUENTIAL** Projection Step: Repeat above



Identifying Pfizer Stoichiometries Additive error = 0.005 on Concentrations $0.005 < C_i(t_k) < 0.9$

Scores of					
Irue reactions					
1	$A + B \leftrightarrows C + D$	96.5			
2	$C \rightarrow D + E$	90.8			
3	$E \rightarrow F$	92.3			
4	B + D ≒ G	99.1			
5	$G \rightarrow D + H$	96.3			
6	$A + F \rightarrow I$	82.4			
7	$2A \rightarrow J$	77.4			
8	$B + J \rightarrow 2E + I$	24.8			

Scores of Untrue reactions				
1	$A \rightarrow J$	57.6		
2	$C \rightarrow J$	38.8		
3	$2A + B \rightarrow J$	72.5		
4	$J \rightarrow 2D + I$	65.0		
5	$B + J \rightarrow E + I$	21.2		
6	$B + J \rightarrow D + I$	51.2		

Blind Test: Excellent Result

Score_i=100(1 - $||\mathbf{n}_{ir} - n_i|| / ||\mathbf{n}_i||$) \mathbf{n}_i = Candidate Stoichiometry \mathbf{n}_{ir} = Response Vector

Seven (7) Significant SVs via an *F*-test $\sigma_i = 81, 9.7, 6.3, 1.5, 1.0, 0.92, 0.22, 0.18, 0.15, 0.09$

Dw



Identifying Pfizer Stoichiometries

NO Measurement error

Scores of True reactions (Without Measurements Error)			Scores of Untrue reactions (Without Measurement error)			
1	$A + B \leftrightarrows C + D$	99.5	1	$A \rightarrow J$	74.6	
2	$C \rightarrow D + E$	99.0	2	$C \rightarrow J$	57.3	
3	$E \rightarrow F$	99.5	3	$2A + B \rightarrow J$	81.9	
4	B + D ≒ G	99.9	4	$J \rightarrow 2D + I$	82.0	
5	$G \rightarrow D + H$	99.5	5	$B + J \rightarrow E + I$	85.8	
6	$A + F \rightarrow I$	99.9	6	$B + J \rightarrow D + I$	88.6	
7	$2A \rightarrow J$	97.9				
8	$B + J \rightarrow 2E + I$	92.7	Confirmation of Method			

Eight (8) Significant SVs σ_i = **81, 9.7, 6.3, 1.5, 1.0, 0.91, 0.19, 0.10**, 0.04, 0.02





Process Optimization via DRSM

Calculate Operating Window (OW):

- Concentrations of Impurities Below Specs
 - Reactants
 - Intermediates

Unwanted by-products

Maximize OW by Selecting
 Operating Conditions
 Account for Uncertainties

Peak or Area HPLC Data





Maximize Operating Window

Optimization Results

• When $\delta_s = 0.1$ for all species,

window does not exist.

Study different specifications

δ_s	Factor1	Factor2	Factor3	Optimal window (hr)
0.14		Infeasible		
0.15	90	1.02	0	3.07
0.16	90	1.03	0.06	4.35
0.17	90	1.03	0.17	4.59
0.18	90	1.03	0.28	4.81
0.19	90	1.03	0.39	5.01
0.2	90	1.03	0.50	5.20





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What to Remember Tomorrow

The Novelty of DoDE and DRSM TWO Generalizations of DoE and RSM DoDE: Experiments with Time Varying Inputs DRSM: Modeling Time-Varying Outputs Stoichiometric Identification Enhanced Some Current Issues Implications of Unmeasured Species Not Enough Candidate Stoichiometries

Thank You Very Much May I answer your Questions